

Table S1: Comparative analysis of self-alignment programs

Genome	Genome length (bp)	Program	Number of matches	Length on the genome (bp)	Genome coverage
<i>D. mel.</i>	129,919,500	BLASTER	109,882	9,636,659	7.41%
		PALS	105,059	9,590,737	7.38%
<i>A. tha.</i>	119,146,348	BLASTER	103,728	16,063,506	13.48%
		PALS	51,023	12,547,315	10.53%